

GAP of: 0964sid2 check: 7022 from: 1 to: 405

WPDEF Case 0964 Rad23 SEQ ID NO: 2 corn

Case 0964 Rad23 SEQ ID NO: 2 corn

to: 0964DY12013aa check: 506 from: 1 to: 382

WPDEF Case 0964D Rad23 protein encoded by GenBank Y12013 carrot

Case 0964D Rad23 protein encoded by GenBank Y12013 carrot

Y12013. *Daucus carota* mRNA. . .[gi:1914682] Links

LOCUS DCRAD23I 1496 bp mRNA linear PLN 28-JAN-1999

DEFINITION *Daucus carota* mRNA for RAD23 protein, isoform I.

ACCESSION Y12013 . . .

Symbol comparison table: /app/gcg/10.2/gcgcore/data/rundata/blosum62.cmp

CompCheck: 1102

BLOSUM62 amino acid substitution matrix.

Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid substitution matrices from protein blocks. *Proc. Natl. Acad. Sci. USA* 89: 10915-10919.

Gap Weight:	8	Average Match:	2.778
Length Weight:	2	Average Mismatch:	-2.248

Quality:	1169	Length:	407
Ratio:	3.060	Gaps:	8
Percent Similarity:	71.053	Percent Identity:	65.789

Match display thresholds for the alignment(s):

	=	IDENTITY
:	=	2
.	=	1

0964sid2 x 0964DY12013aa March 31, 2003 14:17 ..

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      .
1 MKLNVKTLKGTNFEIEASPDASVADV KRIIETTQGGSTYRADQQMLIYQG 50
  ||: |||||. |||: .|| ||||| ||| || . | | |||||
1 MKIYVKTLKGSQFEIQVNPDDSVADV KRSIETAQGAAYVPAQQMLIYQG 50
      .
      .
      .
51 KILKDETTLESNGVAENSFLVIMLSKAKASSSGASTATTAKAPATLAQPA 100
  |:||| ||| | |||||:|||||.|. | || .|| || |
51 KVLKDGTTLLENNVAENSFIVIMLSKSKSPSGEGSTTSTAAAPKAPQTS 100
      .
      .
      .
101 APVAPAASVARTPTQA.PVATAETAPPSVQPQAAPAATVAATDDADVYSQ 149
  | || .|. | || || || | || . | :|.||
101 PPSVPAPAVSQPPASTLPVPAPSPAP...APATAPIPSAAVGSEANVYDS 147
      .
      .
      .
150 AASNLVFGNNLEQTIQQIILDMGGGTWERDTVVRALRAAYNNPERAIDYLY 199
  ||| || |.||| |||||:||||:| .||:|||||:|
148 AASLLVAGSNLEGAIQQIILDMGGGTWDRDTVIRIVRAAFNNPERAVEYLY 197
      .
      .
      .
200 SGIPENVEAQPVARAPAAGQQTNQQAASPA.QPAVALPVQPSPASAGPNA 248
  ||||| || ||| .| .| |||. | || | ||.|||||
198 SGIPEQAEAPPVAPSPPSG.....QAANPLDQPPAA..AQPA PASAGPNA 240
      .
      .
      .

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249 NPLNLFPGVPSGGSNPGVVPGAGSGALDALRQLPQFQALLQLVQANPQI 298  
| | | . | | | | | . | | | | | | | | | | | | | | | : | | . | | | |  
241 NPLDLFPQGLPDMGSN . . . . . AAGAGNLDFLRTNQQFQALRAMVQSNPQI 285  
299 LQPMLQELGKQNPQILRLIQENQAEFLRLVNESPEGGPGGNILGQLAAAV 348  
| | | | | | | | | | | | : | | | | | . | | : | | . | : | | | | | | | : | |  
286 LQPMLQELGKQNPFLMRLIQEHQADFLQLINEPMEGGE . . NLLGH . . . . G 329  
349 PQTLTVTPEEREAIQRLEGMGFNRELVLEVFFACNKDEELTANYLLDGH 398  
| | : . | | | | | : | | : | | | | | . | | | | | | | | | | | | | | | | | | | | | | |  
330 PQAISVTPEERDAIERLEAMGFDRELVLEVFFACNKNEELAANYLLDHMH 379  
399 EFDDQQQ 405  
| | :  
380 EFE . . . . 382